

Notice of Allowability

Application No.

09/865,090

Examiner

John S. Brusca

Applicant(s)

GARNER ET AL.

Art Unit

1631

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address--

All claims being allowable, PROSECUTION ON THE MERITS IS (OR REMAINS) CLOSED in this application. If not included herewith (or previously mailed), a Notice of Allowance (PTOL-85) or other appropriate communication will be mailed in due course. **THIS NOTICE OF ALLOWABILITY IS NOT A GRANT OF PATENT RIGHTS.** This application is subject to withdrawal from issue at the initiative of the Office or upon petition by the applicant. See 37 CFR 1.313 and MPEP 1308.

1. ☒ This communication is responsive to the submission after final filed 06 December 2005 and the interview of 20 December 2005.

2. ☒ The allowed claim(s) is/are 1-4,6 and 8-23.

3. ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a) ☐ All b) ☐ Some* c) ☐ None of the:

1. ☐ Certified copies of the priority documents have been received.

2. ☐ Certified copies of the priority documents have been received in Application No. _____.

3. ☐ Copies of the certified copies of the priority documents have been received in this national stage application from the International Bureau (PCT Rule 17.2(a)).

* Certified copies not received: _____.

Applicant has THREE MONTHS FROM THE "MAILING DATE" of this communication to file a reply complying with the requirements noted below. Failure to timely comply will result in ABANDONMENT of this application.

THIS THREE-MONTH PERIOD IS NOT EXTENDABLE.

4. ☐ A SUBSTITUTE OATH OR DECLARATION must be submitted. Note the attached EXAMINER'S AMENDMENT or NOTICE OF INFORMAL PATENT APPLICATION (PTO-152) which gives reason(s) why the oath or declaration is deficient.

5. ☐ CORRECTED DRAWINGS (as "replacement sheets") must be submitted.

(a) ☐ including changes required by the Notice of Draftsperson's Patent Drawing Review (PTO-948) attached

1) ☐ hereto or 2) ☐ to Paper No./Mail Date _____.

(b) ☐ including changes required by the attached Examiner's Amendment / Comment or in the Office action of Paper No./Mail Date _____.

Identifying indicia such as the application number (see 37 CFR 1.84(c)) should be written on the drawings in the front (not the back) of each sheet. Replacement sheet(s) should be labeled as such in the header according to 37 CFR 1.121(d).

6. ☐ DEPOSIT OF and/or INFORMATION about the deposit of BIOLOGICAL MATERIAL must be submitted. Note the attached Examiner's comment regarding REQUIREMENT FOR THE DEPOSIT OF BIOLOGICAL MATERIAL.

Attachment(s)

1. ☒ Notice of References Cited (PTO-892)

2. ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)

3. ☐ Information Disclosure Statements (PTO-1449 or PTO/SB/08),
Paper No./Mail Date _____

4. ☐ Examiner's Comment Regarding Requirement for Deposit
of Biological Material

5. ☐ Notice of Informal Patent Application (PTO-152)

6. ☐ Interview Summary (PTO-413),
Paper No./Mail Date _____

7. ☒ Examiner's Amendment/Comment

8. ☒ Examiner's Statement of Reasons for Allowance

9. ☐ Other _____.

EXAMINER'S AMENDMENT

1. An examiner's amendment to the record appears below. Should the changes and/or additions be unacceptable to applicant, an amendment may be filed as provided by 37 CFR 1.312. To ensure consideration of such an amendment, it **MUST** be submitted no later than the payment of the issue fee.

Authorization for this examiner's amendment was given in a telephone interview with Richard Aron Osmon on 20 December 2005.

The application has been amended as follows:

A new complete claim listing is provided beginning on the next page which incorporates the examiner's amendment.

Art Unit: 1631

1. (Currently Amended) A computer-based system for creating from one or more a datasets a data table comprising sequence identifiers corresponding to a targeted collection of sequences , the one or more datasets comprising sequence identifiers corresponding to biopolymer sequences and linked to corresponding annotations, the system comprising:

a) a search function which searches the annotations of the one or more datasets according to one or more a user-defined criteria~~en~~ and outputs a first subset of the one or more datasets restricted by the one or more criteria~~en~~;

b) a redundancy reducing function which compares the first subset with a one or more first databases correlating the sequence identifiers of the first subset with common source gene biopolymers and outputs a second subset of the dataset having reduced ~~unique~~ biopolymer redundancy relative to the first subset;

c) a selection function which applies to the second subset a user-defined selection parameter and outputs a third subset of the one or more datasets restricted relative to the second subset by the parameter; and

d) a tabulation function which creates and outputs the targeted collection of sequences in the form of a data table comprising, configurable by and sortable by the sequence identifiers of the third subset.

2. (Currently Amended) A system according to claim 1, wherein the one or more criteria~~en~~ is selected from the group consisting of a keyword and a concept.

Art Unit: 1631

3. (Currently Amended) A system according to claim 1, wherein the one or more criteria~~aen~~ is one of a plurality of user-defined criteria, and the search function searches the annotations of the one or more datasets according to the one or more criteria and outputs a first subset of the one or more datasets restricted by the one or more criteria.

4. (Currently Amended) A system according to claim 1, wherein the one or more criteria~~aen~~ is one of a plurality of user-defined criteria, and the search function searches the annotations of the one or more datasets according to the one or more criteria and outputs a first subset of the one or more datasets restricted by the one or more criteria, wherein the one or more criteria include multiple keywords.

5. (Canceled)

6. (Currently Amended) A system according to claim 1, wherein the one or more datasets is one of a plurality of datasets, and the search function searches the annotations of the one or more datasets according to the one or more user-defined criteria~~aen~~ and outputs a first subset of the one or more datasets restricted by the one or more criteria~~aen~~.

7. (Canceled)

8. (Currently Amended) A system according to claim 1, wherein the one or more first databases is one of a plurality of databases correlating the sequence identifiers of the first subset with

Art Unit: 1631

common source gene biopolymers, and the redundancy reducing function compares the first subset with the one or more first databases and outputs the second subset of the one or more datasets.

9. (Previously presented) A system according to claim 1, wherein the parameter is selected from the group consisting of source, species, author, and pathway.

10. (Original) A system according to claim 1, wherein the parameter is one of a plurality of user-defined selection parameters, and the selection function applies to the second subset the parameters and outputs the third subset restricted relative to the second subset by the parameters.

11. (Currently Amended) A system according to claim 1, wherein the redundancy reducing function outputs a second subset of the one or more datasets which eliminates ~~unique~~ biopolymer redundancy relative to the first subset.

12. (Original) A system according to claim 1, further comprising an expansion function which searches a second database for synonyms of the sequence identifiers of the first, second or third subset.

13. (Currently amended) A computer-based method for creating from a dataset a data table comprising sequence identifiers corresponding to a targeted collection of sequences the dataset

Art Unit: 1631

comprising sequence identifiers corresponding to biopolymer sequences and linked to corresponding annotations, the method comprising computer-implemented steps of:

- a) searching with a computer the annotations of the dataset according to a user-defined criterion and outputting a first subset of the dataset restricted by the criterion;
- b) comparing with the computer the first subset with a database correlating the sequence identifiers of the first subset with common source gene biopolymers and outputting a second subset of the dataset having reduced ~~unique~~ biopolymer redundancy relative to the first subset;
- c) applying to the second subset a user-defined selection parameter and outputting a third subset of the dataset restricted relative to the second subset by the parameter; and
- d) creating and outputting the targeted collection of sequences in the form of a data table comprising, configurable by and sortable by the sequence identifiers of the third subset

14. (Currently amended) A computer-based system for creating from a plurality of datasets a data table comprising sequence identifiers corresponding to a targeted collection of sequences , the datasets comprising sequence identifiers corresponding to biopolymer sequences, the system comprising:

- a) a merge and redundancy reducing function which compares the datasets with a database correlating the sequence identifiers with common source gene biopolymers and creates a subset of the sum of the datasets having reduced ~~unique~~ biopolymer redundancy relative to the sum; and

b) a tabulation function which creates and outputs the targeted collection of sequences in the form of a data table comprising, configurable by and sortable by the sequence identifiers of the subset.

15. (Original) A system according to claim 14, wherein the merge and redundancy reducing function further comprises a selection function which applies a user-defined selection parameter whereby the subset is restricted relative to the sum of the datasets by the parameter.

16. (Previously presented) A system according to claim 14, wherein the merge and redundancy reducing function further comprises a selection function which applies a user-defined selection parameter whereby the subset is restricted relative to the sum of the datasets by the parameter, wherein the parameter is selected from the group consisting of source, author, and pathway.

17. (Currently amended) A computer-based method for creating from a plurality of datasets a data table comprising sequence identifiers corresponding to a targeted collection of sequences, the datasets comprising sequence identifiers corresponding to biopolymer sequences, the method comprising computer-implemented steps of:

a) comparing the datasets with a database correlating the sequence identifiers with common source gene biopolymers and creating a subset of the sum of the datasets having reduced ~~unique~~ biopolymer redundancy relative to the sum; and

b) creating and outputting the targeted collection of sequences in the form of a data table comprising, configurable by and sortable by the sequence identifiers of the subset.

18. (Previously presented) A computer-based system for creating from a dataset a data table comprising sequence identifiers corresponding to a targeted collection of sequences, the dataset comprising sequence identifiers corresponding to biopolymer sequences and linked to corresponding first annotations, the system comprising:

a) an integration function which merges the dataset with a database comprising second annotations attributable to and correlated with at least a subset of the sequence identifiers or sequences of the dataset and which links the second annotations to the corresponding sequence identifiers of the subset; and

b) a tabulation function which creates and outputs the targeted collection of sequences in the form of a data table comprising, configurable by and sortable by the sequence identifiers of the subset and the second annotations.

19. (Original) A system according to claim 18, wherein the second annotations comprise data attributable to and correlated with at least a subset of the sequence identifiers or sequences of the dataset, said data selected from the group consisting of: gene expression data, sequencing data, genotype data, polymorphism data and clinical data.

20. (Previously presented) A computer-based method for creating from a dataset a data table comprising sequence identifiers corresponding to a targeted collection of sequences, the dataset comprising sequence identifiers corresponding to biopolymer sequences and linked to corresponding first annotations, the method comprising computer-implemented steps of:

Art Unit: 1631

a) merging the dataset with a database comprising second annotations attributable to and correlated with at least a subset of the sequence identifiers or sequences of the dataset and linking the second annotations to the corresponding sequence identifiers of the subset; and

b) creating and outputting the targeted collection of sequences in the form of a data table comprising, configurable by and sortable by the sequence identifiers of the subset and the second annotations.

21. (Currently amended) A system according to claim 1, further comprising:

a second computer-based system for creating from a plurality of datasets a data table comprising sequence identifiers corresponding to a targeted collection of sequences, the datasets comprising sequence identifiers corresponding to biopolymer sequences, the second system comprising:

a) a merge and redundancy reducing function which compares the datasets with a database correlating the sequence identifiers with common source gene biopolymers and creates a subset of the sum of the datasets having reduced ~~unique~~ biopolymer redundancy relative to the sum; and

b) a tabulation function which creates and outputs the targeted collection of sequences in the form of a data table comprising, configurable by and sortable by the sequence identifiers of the subset.

22. (Previously presented) A system according to claim 1, further comprising:

Art Unit: 1631

a second computer-based system for creating from a dataset a data table comprising sequence identifiers corresponding to a targeted collection of sequences, the dataset comprising sequence identifiers corresponding to biopolymer sequences and linked to corresponding first annotations, the second system comprising:

a) an integration function which merges the dataset with a database comprising second annotations attributable to and correlated with at least a subset of the sequence identifiers or sequences of the dataset and which links the second annotations to the corresponding sequence identifiers of the subset; and

b) a tabulation function which creates and outputs the targeted collection of sequences in the form of a data table comprising, configurable by and sortable by the sequence identifiers of the subset and the second annotations.

23. (Currently amended) A system according to claim 1, further comprising:

a second computer-based system for creating from a plurality of datasets a data table comprising sequence identifiers corresponding to a targeted collection of sequences, the datasets comprising sequence identifiers corresponding to biopolymer sequences, the second system comprising:

a) a merge and redundancy reducing function which compares the datasets with a database correlating the sequence identifiers with common source gene biopolymers and creates a subset of the sum of the datasets having reduced ~~unique~~ biopolymer redundancy relative to the sum; and

Art Unit: 1631

b) a tabulation function which creates and outputs the targeted collection of sequences in the form of a data table comprising, configurable by and sortable by the sequence identifiers of the subset; and,

a third computer-based system for creating a targeted collection of sequences from a dataset comprising sequence identifiers corresponding to biopolymer sequences and linked to corresponding first annotations, the third system comprising:

a) an integration function which merges the dataset with a database comprising second annotations attributable to and correlated with at least a subset of the sequence identifiers or sequences of the dataset and which links the second annotations to the corresponding sequence identifiers of the subset; and

b) a tabulation function which creates and outputs the targeted collection of sequences in the form of a data table comprising, configurable by and sortable by the sequence identifiers of the subset and the second annotations.

24. (Canceled)

2. The following is an examiner's statement of reasons for allowance: The closest publication is Kulkarni et al. which reviews the prior art and details many aspects of the instant claimed invention. Kulkarni et al. is not prior art. The Kulkarni et al. authorship includes the two instant inventors. The prior art does not show a database method that searches annotations associated with a biopolymer in a database, reduces redundancy with reference to sequence identifiers associated with the biopolymer, searches the resulting data by a parameter, and outputs the result.

Any comments considered necessary by applicant must be submitted no later than the payment of the issue fee and, to avoid processing delays, should preferably accompany the issue fee. Such submissions should be clearly labeled "Comments on Statement of Reasons for Allowance."

Conclusion

3. Patent applicants with problems or questions regarding electronic images that can be viewed in the Patent Application Information Retrieval system (PAIR) can now contact the USPTO's Patent Electronic Business Center (Patent EBC) for assistance. Representatives are available to answer your questions daily from 6 am to midnight (EST). The toll free number is (866) 217-9197. When calling please have your application serial or patent number, the type of document you are having an image problem with, the number of pages and the specific nature of the problem. The Patent Electronic Business Center will notify applicants of the resolution of the problem within 5-7 business days. Applicants can also check PAIR to confirm that the problem has been corrected. The USPTO's Patent Electronic Business Center is a complete

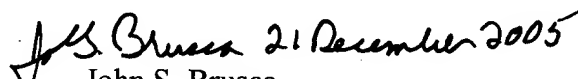
Art Unit: 1631

service center supporting all patent business on the Internet. The USPTO's PAIR system provides Internet-based access to patent application status and history information. It also enables applicants to view the scanned images of their own application file folder(s) as well as general patent information available to the public.

For all other customer support, please call the USPTO Call Center at (800) 786-9199. Any inquiry concerning this communication or earlier communications from the examiner should be directed to John S. Brusca whose telephone number is 571 272-0714. The examiner can normally be reached on M-F 8:30 AM - 5:00 PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ardin Marschel, PhD. can be reached on 571 272-0718. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).


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Primary Examiner
Art Unit 1631

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